



#5

SEQUENCE LISTING

<110> de Lanerolle, Primal
Nowak, Grzegorz
Pestic-Dragovich, Lidiya
Stojiljkovic, Ljuba
Hozak, Pavel

<120> Nuclear Myosin I B with A 16 Amino Acid N-Terminal
Extension

<130> 30151/92399

<140> 09/893,371

<141> 2001-06-27

<150> 60/214,944

<151> 2000-06-29

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1044

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Nuclear Myosin
1 beta

<400> 1

Met Arg Tyr Arg Ala Ser Ala Leu Gly Ser Asp Gly Val Arg Val Thr
1 5 10 15

Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val Gln Asp Phe
20 25 30

Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile Glu Asn Leu
35 40 45

Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile Gly Pro Val
50 55 60

Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr Ser Arg Gln
65 70 75 80

Arg Lys Ile Ile Ala Lys Gly Glu Glu Leu Leu Ser Pro Leu Asn Leu
 340 345 350

Glu Gln Ala Ala Tyr Ala Arg Asp Ala Leu Ala Lys Ala Val Tyr Ser
 355 360 365

Arg Thr Phe Thr Trp Leu Val Arg Lys Ile Asn Arg Ser Leu Ala Ser
 370 375 380

Lys Asp Ala Glu Ser Pro Ser Trp Arg Ser Thr Thr Val Leu Gly Leu
 385 390 395 400

Leu Asp Ile Tyr Gly Phe Glu Val Phe Gln His Asn Ser Phe Glu Gln
 405 410 415

Phe Cys Ile Asn Tyr Cys Asn Glu Lys Leu Gln Gln Leu Phe Ile Glu
 420 425 430

Leu Thr Leu Lys Ser Glu Gln Glu Glu Tyr Glu Ala Glu Gly Ile Ala
 435 440 445

Trp Glu Pro Val Gln Tyr Phe Asn Asn Lys Ile Ile Cys Asp Leu Val
 450 455 460

Glu Glu Lys Phe Lys Gly Ile Ile Ser Ile Leu Asp Glu Glu Cys Leu
 465 470 475 480

Arg Pro Gly Glu Ala Thr Asp Leu Thr Phe Leu Glu Lys Leu Glu Asp
 485 490 495

Thr Val Lys Pro His Pro His Phe Leu Thr His Lys Leu Ala Asp Gln
 500 505 510

Lys Thr Arg Lys Ser Leu Asp Arg Gly Glu Phe Arg Leu Leu His Tyr
 515 520 525

Ala Gly Glu Val Thr Tyr Ser Val Thr Gly Phe Leu Asp Lys Asn Asn
 530 535 540

Asp Leu Leu Phe Arg Asn Leu Lys Glu Thr Met Cys Ser Ser Met Asn
 545 550 555 560

Pro Ile Met Ala Gln Cys Phe Asp Lys Ser Glu Leu Ser Asp Lys Lys
 565 570 575

Arg Pro Glu Thr Val Ala Thr Gln Phe Lys Met Ser Leu Leu Gln Leu
 580 585 590

Val Glu Ile Leu Arg Ser Lys Glu Pro Ala Tyr Ile Arg Cys Ile Lys
 595 600 605

Pro Asn Asp Ala Lys Gln Pro Gly Arg Phe Asp Glu Val Leu Ile Arg
 610 615 620

His Gln Val Lys Tyr Leu Gly Leu Met Glu Asn Leu Arg Val Arg Arg
 625 630 635 640

Ala Gly Phe Ala Tyr Arg Arg Lys Tyr Glu Ala Phe Leu Gln Arg Tyr
 645 650 655

Lys Ser Leu Cys Pro Glu Thr Trp Pro Met Trp Ala Gly Arg Pro Gln
 660 665 670

Asp Gly Val Ala Val Leu Val Arg His Leu Gly Tyr Lys Pro Glu Glu
 675 680 685

Tyr Lys Met Gly Arg Thr Lys Ile Phe Ile Arg Phe Pro Lys Thr Leu
 690 695 700

Phe Ala Thr Glu Asp Ser Leu Glu Val Arg Arg Gln Ser Leu Ala Thr
 705 710 715 720

Lys Ile Gln Ala Ala Trp Arg Gly Phe His Trp Arg Gln Lys Phe Leu
 725 730 735

Arg Val Lys Arg Ser Ala Ile Cys Ile Gln Ser Trp Trp Arg Gly Thr
 740 745 750

Leu Gly Arg Arg Lys Ala Ala Lys Arg Lys Trp Ala Ala Gln Thr Ile
 755 760 765

Arg Arg Leu Ile Arg Gly Phe Ile Leu Arg His Ser Pro Arg Cys Pro
 770 775 780

Glu Asn Ala Phe Phe Leu Asp His Val Arg Ala Ser Phe Leu Leu Asn
 785 790 795 800

Leu Arg Arg Gln Leu Pro Arg Asn Val Leu Asp Thr Ser Trp Pro Thr
 805 810 815

Pro Pro Pro Ala Leu Arg Glu Ala Ser Glu Leu Leu Arg Glu Leu Cys
 820 825 830

Met Lys Asn Met Val Trp Lys Tyr Cys Arg Ser Ile Ser Pro Glu Trp
 835 840 845

Lys Gln Gln Leu Gln Gln Lys Ala Val Ala Ser Glu Ile Phe Lys Gly
850 855 860

Lys Lys Asp Asn Tyr Pro Gln Ser Val Pro Arg Leu Phe Ile Ser Thr
865 870 875 880

Arg Leu Gly Thr Glu Glu Ile Ser Pro Arg Val Leu Gln Ser Leu Gly
885 890 895

Ser Glu Pro Ile Gln Tyr Ala Val Pro Val Val Lys Tyr Asp Arg Lys
900 905 910

Gly Tyr Lys Pro Arg Pro Arg Gln Leu Leu Leu Thr Pro Ser Ala Val
915 920 925

Val Ile Val Glu Asp Ala Lys Val Lys Gln Arg Ile Asp Tyr Ala Asn
930 935 940

Leu Thr Gly Ile Ser Val Ser Ser Leu Ser Asp Ser Leu Phe Val Leu
945 950 955 960

His Val Gln Arg Glu Asp Asn Lys Gln Lys Gly Asp Val Val Leu Gln
965 970 975

Ser Asp His Val Ile Glu Thr Leu Thr Lys Thr Ala Leu Ser Ala Asp
980 985 990

Arg Val Asn Asn Ile Asn Ile Asn Gln Gly Ser Ile Thr Phe Ala Gly
995 1000 1005

Gly Pro Gly Arg Asp Gly Ile Ile Asp Phe Thr Ser Gly Ser Glu Leu
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Leu Asn Ser Arg

<210> 2

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:N-terminal 16
amino acid extension

<400> 2

Met Arg Tyr Arg Ala Ser Ala Leu Gly Ser Asp Gly Val Arg Val Thr
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<210> 3

<211> 3661

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:NMI Beta

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<210> 4

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:NMI Beta
 Peptide Overlapping Consensus Start Site

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Leu Thr Ala Arg
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<210> 5
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Myosin I primer

<400> 5
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22

<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Adapter primer

<400> 6
ccatcctaatac gactcact atagggc

27